SEQUENCE LISTING

- (1) GENERAL INFORMATION
 - (i) APPLICANT: Horwath, K. L., et al.
 - (ii) TITLE OF INVENTION: Nucleic Acids Sequences Encoding Type III Tenebrio Antifreeze Proteins and Method for Assaying Activity.
 - (iii) NUMBER OF SEQUENCES: 48
 - (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSEE: Dr. Kathleen L. Horwath
 - (B) STREET: Department of Biological Sciences, Binghamton University
 - (C) CITY: Binghamton
 - (D) STATE: New York
 - (E) ZIP: 13902-6000
 - (v) COMPUTER READABLE FORM
 - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 - (B) COMPUTER: IBM AT/ATX compatible
 - (C) OPERATING SYSTEM: Windows 95/98
 - (D)SOFTWARE: Microsoft Word
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA
 - (A) APPLICATION NUMBER: 60210446
 - (B) FILING DATE: June 8, 2000
 - (viii) ATTORNEY/AGENT INFORMATION
 - (A) NAME: Mark Levy, Attorney-at-Law
 - (B) REGISTRATION NUMBER: 29-188
 - (C) REFERENCE/DOCKET NUMBER: RB125
 - (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: 607-722-6600
 - (B) TELEFAX: 607-724-2207

- (2) INFORMATION FOR SEQ. ID NO: 1
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Peptide
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) FRAGMENT TYPE: N-terminal fragment
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
 - (ix) FEATURES:
 - (D) OTHER INFORMATION: N-terminal sequence of protein Tm 12.86
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val

(2) INFORMATION FOR SEQ. ID NO: 2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 566 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double(D) TOPOLOGY: linear(ii) MOLECULE TYPE: cDNA to mRNA	
<pre>(iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE:</pre>	
(A) ORGANISM: Tenebrio molitor(B) INDIVIDUAL/ISOLATE: none(C) CELL TYPE: fat body and whole organism	
(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA	
(B) CLONE: 13.17 (ix)FEATURES (D) OTHER INFORMATION: Non-his-tagged, signa	l plus
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
GTGGATCCAA AGAATTCGGC ACGAGACTAC TAAG ATG AAG TTG Met Lys Leu	
TGT TGT CTA ATC TCC CTC ATT CTG TTG GTC ACA GTT CAG GCC Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val Gln Ala I	
ACC GAG GCA CAA ATT GAG AAA CTG AAC AAG ATC AGC AAA AAA Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys 5 10 15	
CAA AAT GAA AGT GGA GTG TCG CAA GAG ATC ATA ACC AAA GCT Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala 20 25 30	
AAC GGT GAC TGG GAG GAC GAT CCT AAA CTG AAA CGC CAA GTT T Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val 1 35 40 45	
TGC GTG GCC AGG AAC GCC GGT CTG GCC ACG GAA TCG GGA GAG Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu 50 55 60	
GTG GTC GAC GTG TTG AGG GAG AAG GTG AGG AAG GTC ACT GAC Val Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp 65 70 75	
GAC GAA GAA ACT GAG AAA ATC ATC AAT AAG TGC GCC GTC AAG ASp Glu Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys 80 85 90	
GAT ACT GTT GAA GAG ACG GTG TTC AAT ACT TTC AAA TGT GTC ASP Thr Val Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val 95	
AAA AAC AAG CCA AAG TTC TCA CCA GTT GAT TGA ACCACCACGA Lys Asn Lys Pro Lys Phe Ser Pro Val Asp * 115	439
CTAGTAGATG GTTCAAATGG TGTGCTTTAC ATATAAAAAT AAAGTGTTTC	489
TGATGTAAAA AAAAAAAAA AAAAAAAAA AACTCGAGAG TATTCTAGAG	539
CGGCCGCGG CCCATCGTTT TCCACCC	566

- (2) INFORMATION FOR SEQ. ID NO: 3 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 134 Amino Acids
 - (B) TYPE: Amino Acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Precursor Protein for Tm 13.17
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
- Met Lys Leu Leu Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val
- Gln Ala Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys
- Lys Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala
- Arg Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe
- Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val
- Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu
- Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val
- Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro

Lys Phe Ser Pro Val Asp * 115

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(2) INFORMATION FOR SEQ. ID NO: 4
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 116 Amino Acids
            (B) TYPE: Amino Acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: Protein
      (iii) HYPOTHETICAL: no
      (iv) ANTI-SENSE: no
      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Tenebrio molitor
            (B) INDIVIDUAL/ISOLATE: none
            (C) CELL TYPE: fat body and whole organism
      (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: cDNA
            (B) CLONE: 13.17
      (ix)FEATURES
            (D) OTHER INFORMATION: Mature Protein for Tm 13.17
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn
Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val
Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Asp
Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr
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Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu

Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe

700

(5)		ii) S(iii) (iii) iv) (vi) (vii)	EQUEN (A) (B) (C) (D) MOLE(HYP(ANTI- ORIGE (A) (B) (C) IMME (A) (B) EATUR	NCE (LENG TYPE STR, TOP(CULE OTHE: SCHOOL ORG, INAL ORG, IND: CELI EDIA; CLOR RES OTHE	CHARASTH: E: ni ANDE OLOGO TYPE TICAL SE: i SOUF ANIST IVIDU L TYPE TE SO RARY: RARY: RE: 6	RCE: 1: Te JAL/1 PE: 1 DURCE : cDi 2:2	RIST: base ic ac ic ac ic ac inear i	ICS: pa cid cubl coubl c	e RNA moli nond and	e who: His-1	tagge			al pl	us
GGC	ACGA	GCA /				CTC (Leu l					Ala ƙ				46
						GCT Ala									91
						GAA Glu 15									136
						GTC Val 30									181
						GTC Val 45									556
						GAC Asp LO									271
						AGC Ser 75									376
						AAG Lys 90									367
	Thr					TAC Tyr 105									406
	100 GAT ASP 115		TTG	ፐፐፐፐር	STA '	TTTG,	ACTG	AA T	TTTG	ACAA'		AGGT	AATA		455
TCG	TTATO	STA A	4 A A A	A A A A	4A A	4444	4								481

(2) INFORMATION FOR SEQ. ID NO: L (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 482 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INDIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and whole organism (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: 2.3 (ix)FEATURES (D) OTHER INFORMATION: Non-His-tagged, Signal plus (xi) SEQUENCE DESCRIPTION: SEQ ID NO: L:	
GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC Met Lys Leu Leu Cys Phe Ala Phe Ala Ala -15 -10	46
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys -5 1 5	91
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser 10 15 20	73P
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30 35	181
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly 40 45 50	5 5 6
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala 55 60	271
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val 70 75 80	316
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr 85 90	367
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro 100 105	406
ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA Ile Asp * Ll5	455

482

TCGTTATGAA AAAAAAAAA AAAAAA

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(2) INFORMATION FOR SEQ. ID NO: 7
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 133 Amino Acids
            (B) TYPE: Amino Acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: Protein
      (iii) HYPOTHETICAL: no
      (iv) ANTI-SENSE: no
      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Tenebrio molitor
            (B) INDIVIDUAL/ISOLATE: none
            (C) CELL TYPE: fat body and whole organism
      (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: cDNA
            (B) CLONE: 2.2, 2.3, and 7.5
      (ix)FEATURES
            (D) OTHER INFORMATION: Precursor Protein for Tm 12.84
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
Met Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
                                -10
            -15
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
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Glu Thr Ala Tyr Asp Thr Phe Lys (ys Ile Tyr Asp Ser Lys Pro Asp

105

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(2) INFORMATION FOR SEQ. ID NO: 8
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 115 Amino Acids
            (B) TYPE: Amino Acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: Protein
      (iii) HYPOTHETICAL: no
      (iv) ANTI-SENSE: no
      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Tenebrio molitor
            (B) INDIVIDUAL/ISOLATE: none
            (C) CELL TYPE: fat body and whole organism
      (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: cDNA
            (B) CLONE: 2.2, 2.3, and 7.5
      (ix)FEATURES
            (D) OTHER INFORMATION: Mature Protein for Tm 12.84
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
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Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser

(ii) SE((iii) M((iii) M((iv) AM((vi) OM((vii) M((vi	IMMEDIATE SOU (A) LIBRARY: (B) CLONE: 3: ATURES	CTERISTICS: 481 base pai cleic acid NESS: double : linear : cDNA to mR : no O CE: : Tenebrio n AL/ISOLATE: E: fat body URCE: cDNA . 4 FORMATION: N	nolitor none and whole or	ganism d _a Signal plus
GGCACGAGCA A			ys Phe Ala Pi	
	GGA GCT CAG (Gly Ala Gln /			
	ATC AGC AAA (Ile Ser Lys (
CAA GAG ACG A Gln Glu Thr 1 25	Ile Asp Lys \			
CCC AAA ATG / Pro Lys Met l 40	Lys Lys His \			
GTG GCA ACC (Val Ala Thr (55	Glu Ala Gly /	GAC ACC AAT Asp Thr Asn bD	GTG GAG GTA (Val Glu Val (65	CTC AAA GCC 271 Leu Lys Ala
AAG CTG AAG (Lys Leu Lys 1 70				
CAG AAG TGC (Gln Lys Cys \ 85	Val Val Lys l			
GAC ACC TTC A Asp Thr Phe L 300	Lys Val Ile 1			
ATT GAT TAA 7 Ile Asp * 115	ттсттттста т	TTGACTGAA TT	TTGACAAT AAA	GGTACTA 455

481

TCGTTATGTA AAAAAAAAA AAAAA

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176
(2) INFORMATION FOR SEQ. ID NO: LO
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 133 Amino Acids
            (B) TYPE: Amino Acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: Protein
      (iii) HYPOTHETICAL: no
      (iv) ANTI-SENSE: no
      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Tenebrio molitor
            (B) INDIVIDUAL/ISOLATE: none
            (C) CELL TYPE: fat body and whole organism
      (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: cDNA
            (B) CLONE: 3.4
      (ix)FEATURES
            (D) OTHER INFORMATION: Precursor Protein for Clone 3.4
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
Met Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
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Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp

105

- (2) INFORMATION FOR SEQ. ID NO: 11
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Mature Protein for Clone 3.4
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
- Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys 10 15
- Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr 20 25 30
- Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe 35 40 45
- Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu 50 60
- Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp 65 70 75 80
- Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr 85 90 95
- Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser
- Pro Ile Asp *

	(2)		ii)	EQUEI (A) (B) (C) (D) MOLE(HYPE ANTI- CRIGO (A) (C) IMMI (A) (B) EATUI	NCE (LENG TYPE STRA TOP(CULE OTHE SENS INAL INAL INDE CELL EDIA CLOM RES OTHE	CHARA STH: CHANDE: ANDE: CHANDE: CHAND	RCE: M: TO UAL/I PE: 1 OURCE : CD! 3.9	RIST bas ic a ic a ic a inea inea inea inea inea inea inea ine	ICS: e pa cid oubl r to m rio: body	e RNA moli non and	e who His-	tagg			al p	lus
	GGC	ACGAO	SCA /				Leu l			TGC Cys		Ala				46
										GAT Asp					AAA Lys	۹1
															TCC Ser	136
															GAT Asp	181
æ															GGA Gly	556
															GCC Ala	271
<u> </u>															GTG Val	316
															TAT Tyr	361
								Asp					Phe		CCT Pro	406
		GAT Asp 115		TTG	TTTT	STA '	ΤΤΤΟ	ACTG	AA T	TTTG	ACAA	T AA	AGGT	АСТА		455
	TCG	ΓΤΑΤ	SAA A	AAA A.	A A A A	4A A	AAAA	AA								482

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179
(2) INFORMATION FOR SEQ. ID NO: 13
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 133 Amino Acids
            (B) TYPE: Amino Acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: Protein
      (iii) HYPOTHETICAL: no
      (iv) ANTI-SENSE: no
      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Tenebrio molitor
            (B) INDIVIDUAL/ISOLATE: none
            (C) (ELL TYPE: fat body and whole organism
      (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: cDNA
            (B) CLONE: 3.9
      (ix)FEATURES
            (D) OTHER INFORMATION: Precursor Protein for Clone 3.9
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
Met Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
            -15
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
Val Glu Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu
Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
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Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp

- (2) INFORMATION FOR SEQ. ID NO: 14
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Mature protein for Clone 3.9 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
- Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
 10 15
- Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr 20 25 30
- Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe 35 40 45
- Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu 50 60
- Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu Val Asp 65 70 75 80
- Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr 85 ' 90 95
- Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
- Pro Ile Asp *

	(5)		ii) Si iii) iii) iv) vii)	EQUE((A) (B) (C) (D) (O) MOLE(HYP(ANTIG((A) (C) (B) (C) (B) (B) (B) (B)	NCE (LENG TYPE STR, TOP(CULE OTHE' -SEN! INAL ORG, IND: CELL EDIA' CLON RES OTHE	CHAR, STH: E: n; ANDE: OLOG' TYPI FICAL SE: I ANISI IVIDI FE SO RARY RE: ER II	RCE: M: Ta UAL/I PE: 1 OURCE CDI 7.5	RIST bas ic as ic	ICS: e pa cid oubl r to m xio ATE: body	e RNA moli non and	e who his-	tagg			al p	lus
	GGC	ACGA	GCA A	4 A A .	ATG / Met l	AAA (_ys	Leu l	CTC Leu -15	TTG Leu	TGC Cys	TTT Phe	Ala	TTC Phe -10	GCC Ala	GCC Ala	46
# F # F # F # F # F # F # F # F # F # F															AAA Lys	90
	AGG Arg	AAC Asn 10	AAG Lys	ATC Ile	AGC Ser	AAA Lys	GAG Glu 15	TGC Cys	CAG Gln	CAG Gln	GTG Val	7CC 20	GGA Gly	6T6 Val	TCC Ser	736
The state of the s															GAT Asp	181
										TTC Phe					GGA Gly	552
															GCC Ala	271
										GAG Glu						37.P
										CCA Pro					TAT Tyr	3P.7
								Asp							CCT Pro	406
		GAT Asp 115		TTG	TTTT	GTA '	TTTG	GCTG	AA T	TTTG	ACAA	T AA	AGGT.	АСТА		455
	TCG	ГТАТ	STA .	A A A	A A A A	AA A	A A A A	A								481

- (2) INFORMATION FOR SEQ. ID NO: 16
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: L&L base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
 - (ix)FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 -20	186
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -10 -5	537
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser 1	276
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp 15 20 25	357
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45 5D 55	411
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys 90 95 100	546
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * LD5 LL5	595
TTTGACTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAA	645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	P8T

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(2) INFORMATION FOR SEQ. ID NO: 17
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
- (ix)FEATURES
- (D) OTHER INFORMATION: Precursor Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro -55
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg ~35
- Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Ceu Cys Phe Ala
- Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
- Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
- Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
- Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
- Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
- Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
- Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
- Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 110

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(2) INFORMATION FOR SEQ. ID NO: 18
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 543 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: cDNA to mRNA
      (iii) HYPOTHETICAL: no
      (iv) ANTI-SENSE: no
      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Tenebrio molitor
            (B) INDIVIDUAL/ISOLATE: none
            (C) CELL TYPE: fat body and whole organism
      (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: cDNA
            (B) CLONE: 2.2
      (ix)FEATURES
            (D) OTHER INFORMATION: His-tagged, signal minus
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: L8:
    TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG
                                                                50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC
                                                                96
               Met Gly Ser Ser His His His His His Ser
                               -30
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT
                                                               1.41.
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
            -50
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG
                                                               186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln
            -5
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG
                                                               537
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
        10
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT
                                                               323
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA
                                                               366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC
                                                               411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT
                                                               456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
                            90
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT
                                                               501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
                            105
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT
                                                               543
Pro Ile Asp *
        115
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(2) INFORMATION FOR SEQ. ID NO: 19
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 149 Amino Acids
            (B) TYPE: Amino Acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: Protein
      (iii) HYPOTHETICAL: no
      (iv) ANTI-SENSE: no
      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Tenebrio molitor
            (B) INDIVIDUAL/ISOLATE: none
            (C) CELL TYPE: fat body and whole organism
      (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: cDNA
            (B) CLONE: 2.2
      (ix)FEATURES
            (D) OTHER INFORMATION: Mature Protein with His-tag
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
```

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp

105

- (2) INFORMATION FOR SEQ. ID NO: 20 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: LAZ base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) (ELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
 - (ix)FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal Plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met ~30 -25 -20	186
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala ~15 -5	531
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser 1	576
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp 15	357
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45	411
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys 90 95 100	546
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 115	595
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAA	645
AAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT	P85

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(2) INFORMATION FOR SEQ. ID NO: 21
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 169 Amino Acids
            (B) TYPE: Amino Acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: Protein
      (iii) HYPOTHETICAL: no
      (iv) ANTI-SENSE: no
      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Tenebrio molitor
            (B) INDIVIDUAL/ISOLATE: none
            (C) CELL TYPE: fat body and whole organism
      (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: cDNA
            (B) CLONE: 2.3
      (ix)FEATURES
            (D) OTHER INFORMATION: Precursor Protein with His-tag
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
                                -50
Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala
Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
-70
Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
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Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys 90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 110

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(2) INFORMATION FOR SEQ. ID NO: 22
          (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 543 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
          (ii) MOLECULE TYPE: cDNA to mRNA
          (iii) HYPOTHETICAL: no
          (iv) ANTI-SENSE: no
          (vi) ORIGINAL SOURCE:
                 (A) ORGANISM: Tenebrio molitor
                 (B) INDIVIDUAL/ISOLATE: none(C) CELL TYPE: fat body and whole organism
          (vii) IMMEDIATE SOURCE:
                 (A) LIBRARY: cDNA
                 (B) CLONE: 2.3
          (ix)FEATURES
                 (D) OTHER INFORMATION: His-tagged, Signal minus
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
        TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG
                                                                     50
    AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC
                                                                     96
                    Met Gly Ser Ser His His His His His Ser
                                    -30
    AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT
                                                                     141
    Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
                 -20
    GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG
    Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln
                 ~5
4
    AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG
    Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
            70
    TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT
                                                                     276
    Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp
    GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT
                                                                     357
    Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr
    GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA
                                                                     366
    Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys
    GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC
                                                                     41,1
    Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile
    GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT
                                                                     456
    Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
                                 90
    TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT
                                                                     501
    Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
                                 702
    CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT
                                                                     543
    Pro Ile Asp *
            115
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(2) INFORMATION FOR SEQ. ID NO: 23
     (i) SEQUENCE CHARACTERISTICS:
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- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (() (ELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
- (ix)FEATURES
- (D) OTHER INFORMATION: Mature Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro -30 ~25
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
- Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
- Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
- Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
- Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
- Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
- Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
- Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp 702 700

- (2) INFORMATION FOR SEQ. ID NO: 24
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (() (ELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix)FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -65 -60 -55	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -50 -45 -40	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile -35 -30 -25	186
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser -20 -15 -10	531
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile -5	276
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly 10 15	357
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu 25 30 35	366
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn 40 45 50	411
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu 55 60 65	45 b
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu 70 75 80	501
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu 85 90 95	54Ь
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys 100 105	595
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG Phe Ser Pro Val Asp * 115	643
TGTGCTTTAC ATATAAAAT AAAGTGTTTC TGATGTAAAA AAAAAAAAA	693
AAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT	743
TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT	777

- (2) INFORMATION FOR SEQ. ID NO: 25
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Precursor Protein with His-tag (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro -50
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg -35
- Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Cys Leu Ile
- Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile
- Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val
- Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp
- Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly Leu
- Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu Lys Val
- Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys
- Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe
- Lys (ys Val Met Lys Asn Lys Pro Lys Phe Ser Pro Val Asp * 110

	(2)	(i (i (i (v	(i) SE (ii) (ii) (v) (vi) (vii)	EQUE (A) (B) (C) (D) 10LE HYP ANTI (A) (C) IMM (B) (A) (B) EATU	NCE (LENG TYPE STRA TOP(CULE OTHE: -SENS INAL ORGA IND: CELL EDIA CLON RES OTHE	CHARA STH: E: nu CANDEI OLOGY TYPE FICAL SE: r SOUR ANISM LVIDL LTYPE FRARY: OR CRARY:	ACTE 543 JC1e NES Y: 1 E: c RCE: n RCE: T JAL DURC URC L3.1	enebi ISOLA fat b E: NA 7	CCS: pa cid cubl co m co m ATE: cody	e RNA moli non and		ed, S			inus	
		TTGT	TAGO	CGG .	ATGG	AATT(c c	TCGTA	AGGG	G AT	AATT	гтст	TTA	CTTT/	AAG	50
	AAG	SAGAT	rat A				Ser				CAT (His H	lis I				96
C U											GCT Ala					141
											GCA Ala					186
											GAA Glu					537
											GAC Asp					276
	Pro	Lys	Leu	Lys	Arg	Gln	Val	Phe	Cys	Val	GCC Ala	Arg	Asn			357
											GAC Asp					366
											GAA Glu					411
											GTT Val					456
								Met			AAG Lys					501
		GTT Val 115			CTC	GAGC	ACC	ACCAG	CCAC	CA C	CACT	SAGA.	Γ			543

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196
(2) INFORMATION FOR SEQ. ID NO: 27
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 149 Amino Acids
            (B) TYPE: Amino Acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: Protein
      (iii) HYPOTHETICAL: no
      (iv) ANTI-SENSE: no
      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Tenebrio molitor
            (B) INDIVIDUAL/ISOLATE: none
            (C) CELL TYPE: fat body and whole organism
      (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: cDNA
            (B) CLONE: 13.17
      (ix)FEATURES
            (D) OTHER INFORMATION: Mature Protein with His-tag
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
            -30
                                -25
Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
Gly Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys
Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg
Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys
Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val
Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu
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Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu 80 85 90 95

Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys

- (2) INFORMATION FOR SEQ. ID NO: 28
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: L&L base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (() (ELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	1,41
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 -20	796
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -10 -5	537
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser L	276
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp 15	357
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45	411
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG GTT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Val 90	546
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 115	595
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAAA	645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	P81

- (2) INFORMATION FOR SEQ. ID NO: 29
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (() (ELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro -50
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
- Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala
- Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
- Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
- Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
- Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
- Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
- Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
- Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
- Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 110

	(5)	() () ()	i) S ii) (iii)	EQUE (A) (B) (C) (D) MOLE HYP	FOR NCE (LENG TYPE STRA TOP(CULE OTHET -SENS	CHARA STH: E: ni ANDE SLOG' TYPE	ACTER 543 ucle: DNES: 1: 1: E: cl	RIST basi ic a S: d S: d inea ANA	ICS: e pai cid ouble	2						
		() ()	vii) (vii) ix) /	(A) (B) (C) IMMI (A) (B) FEATI	INAL ORGA INDI CELL EDIAT LIBF CLON JRES OTHE	ANISI EVIDU TYF TE SC RARY: NE: 3	1: Te JAL/I PE: 1 DURCE CD1 B.4	ISOL, fat E: NA	ATE: Dody ON: 1	none and	e who: tagge	ed₁ :			inus	
		TTG	TTAG	CGG .	ATGGA	TTA	c c'	rcgr	AGGGG	S AT	AATT'	rtgt	TTA	CTTT	AAG	50
atheren.	AAG	SAGA'	ΓΑΤ		ATG (Met (Ser I					lis I			96
					CCG Pro											141
					GGT Gly											186
					ATC Ile											537
					ATC Ile											276
					AAG Lys											351
					GAA Glu											366
					CAT His											411
					<i>GTG</i> Val											456
					AAG Lys											501
		ATT Ile LL5			CTC	SAGCA	ACC /	ACCAG	CCAC	CA C	CACT	SAGA1	r			543

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(2) INFORMATION FOR SEQ. ID NO: 31
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 149 Amino Acids
            (B) TYPE: Amino Acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: Protein
      (iii) HYPOTHETICAL: no
      (iv) ANTI-SENSE: no
      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Tenebrio molitor
            (B) INDIVIDUAL/ISOLATE: none
            (C) CELL TYPE: fat body and whole organism
      (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: cDNA
            (B) CLONE: 3.4
      (ix) FEATURES
            (D) OTHER INFORMATION: Mature Protein with His-tag
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
              -30
                                   -25
Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
```

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp

105

- (2) INFORMATION FOR SEQ. ID NO: 32
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) (ELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25	786
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -10 -5	537
CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser L	276
AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp 15 20 25	357
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 3D 35 40	366
CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala 45	411
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys 90 95 100	546
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * LD5 LLD LL5	595
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAA	645
AAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT	P85

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(2) INFORMATION FOR SEQ. ID NO: 33
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 173 Amino Acids
            (B) TYPE: Amino Acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: Protein
      (iii) HYPOTHETICAL: no
      (iv) ANTI-SENSE: no
      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Tenebrio molitor
            (B) INDIVIDUAL/ISOLATE: none
            (C) CELL TYPE: fat body and whole organism
      (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: cDNA
            (B) CLONE: 3.9
      (ix) FEATURES
            (D) OTHER INFORMATION: Precursor Protein with His-tag
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
                                -50
Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala
Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
-10
Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly Val
Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
Lys HisVal Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
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Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *

770

115

	(2)		ii) Siii) !iii) !iii) !vii) !vii) !vii) !	EQUE (A) (B) (C) (D) MOLE HYP ANTIG (A) (C) IMM (B) FEAT	TYPI STR TOP CULE OTHE SENSINAL ORG IND CELI EDIA CLO URES OTHE	CHAR GTH: E: n ANDE OLOG TYP TICA SE: SOUID ANIS IVID TYP TE S RAP RAP RAP ER I	ACTEL 543 UC1e DNES Y: 1 E: no RCE: DJAL PE: DURCI OURCI OUR	RIST bas ic a S: d inea INA o eneb ISOL fat NA MATI	ICS: e pa: cid ouble r to mf	RNA moli noni and	e who tagg	le or ed, : 34:			inus	
		TTG	TTAG	CGG .	ATGG	AATT	cc c	TCGT	AGGG	SAT	AATT	TTGT	TTA	CTTT	AAG	50
	AAG	GAGA'	TAT /					Ser				CAT (His			96
					Pro							AGC Ser			Gly	141
												GAA Glu				186
												GAG Glu				537
												GTC Val				276
			Lys	Met		Lys	His	Val	Leu	Cys	Phe	TCG Ser				357
												GAG Glu				366
												GTG Val				411
												GAG Glu				456
									Asp			CCT Pro				501
		ATT Ile			CTC	SAGC	ACC A	ACCA	CCAC	CA C	CACT	GAGA'	r			543

- (2) INFORMATION FOR SEQ. ID NO: 35
 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Mature Protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro -30 -25 -20
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg -15 -10 -5
- Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
- Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val 15 20 25 30
- Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu 35 40 45
- Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60
- Val Glu Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu 65 7D 75
- Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu 80 85 90
- Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp 35 100 105

Phe Ser Pro Ile Asp * 115

- (2) INFORMATION FOR SEQ. ID NO: 3L
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: L&L base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) (ELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

		TTG	TTAG	CGG	ATGG	AATT	cc c	TCGT	AGGG	G AT	'AATT	TTGT	TTA	CTTT	AAG	50
	AAG	SAGAT	ΓΑΤ			Gly						CAT His -50				96
								Ser							GGT Gly	141
•								Ser				. CGA . Arg 20	Ala		AT <i>G</i> Met	786
								Phe							GCT Ala	537
												AAC Asn 10			AGC Ser	576
												GAG Glu 25			GAC Asp	357
												AAA Lys 40			AAG Lys	366
y D N												GCA Ala 55				411
and the first first suit												CTG Leu 70			GTG Val	456
												AAG Lys 85			GTC Val	501
					_		~ -					ACC Thr 100			_	546
								Phe				GAT ASP 115		TTG	TTTTGTA	595
	TTTC	GCTO	AA '	TTTT	GACA	AT A	AAGG	ΤΑСΤ	Ά ΤΟ	GTTA	TGTA	. AAA	A A A A	AAA		645
	AAA	AACI	rcg .	AGCA	CCAC	CA C	CACC	ACCA	C TG	AGAT						681

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(2) INFORMATION FOR SEQ. ID NO: 37
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 173 Amino Acids
            (B) TYPE: Amino Acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: Protein
      (iii) HYPOTHETICAL: no
      (iv) ANTI-SENSE: no
      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Tenebrio molitor
            (B) INDIVIDUAL/ISOLATE: none
            (C) CELL TYPE: fat body and whole organism
      (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: cDNA
            (B) CLONE: 7.5
      (ix) FEATURES
            (D) OTHER INFORMATION: Precursor Protein with His-tag
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
                                -50
            ~55
Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala
Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
-70
Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
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Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 110 115

	(2)		ii)	EQUE (A) (B) (C) (D) MOLE HYP ANTI (A) (B) (B) (B) (B)	FOR NCE (LENG TYPE STRA TOP(CULE OTHET -SENS INAL ORGA INDI CELL EDIAT LIBF CLON UNCE ENCE	CHAR. STH: CHANDE CHANDE CHANDS C	ACTER 543 ucle: DNESS Y: l: E: cl L: no RCE: M: Te UAL/I PE: t OURCE TO OURCE NFORI	RIST: base ic ac ic ac ic ac ineae i	ICS: e pa cid oubl c to m rio ATE: body	e RNA molí non and	e who: tagg	ed. :			inus	
		TTGT	TTAG(CGG	ATGG	TTA	cc c.	rcgr	AGGG	G AT	A A T T	TTGT	TTA	ር ፐ ፐ ፐ ፖ	AAG	50
	AAGO	SAGAT	ΓAT A		ATG (Met (Ser I					His I			96
					CCG Pro					Met						141
					GGT Gly											186
					ATC Ile											531
					ATC Ile											276
					AAG Lys											351
					GAA Glu											366
					CAT His											411
					GTG Val											456
					AAG Lys				Asp							501
		Ile			СТС	SAGC	ACC /	ACCA	CCAC	CA C	CACT	GAGA'	Т			543

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(2) INFORMATION FOR SEQ. ID NO: 39
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 149 Amino Acids
            (B) TYPE: Amino Acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: Protein
      (iii) HYPOTHETICAL: no
      (iv) ANTI-SENSE: no
      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Tenebrio molitor
            (B) INDIVIDUAL/ISOLATE: none
            (C) CELL TYPE: fat body and whole organism
      (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: cDNA
            (B) CLONE: 7.5
      (ix) FEATURES
            (D) OTHER INFORMATION: Mature protein with His-tag
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
               -30
                                   ~25
Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
                                        105
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RB125 SEQ

Phe Ser Pro Ile Asp *

115

- (2) INFORMATION FOR SEQ. ID NO: 40
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 12.84 upper primer with Bam-H1 site (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGCGGATCCC TCACCGACGA ACAG

24

- (2) INFORMATION FOR SEQ. ID NO: 41
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism (vii) IMMEDIATE SOURCE:
 - - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 12.84 lower primer with Xhol site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAGGATAA CTAATTGAGC TCGCC

- (2) INFORMATION FOR SEQ. ID NO: 42 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (v) (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor

 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism

24

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
- (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 13.17 upper primer with Bam-H1 site
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CGCGGATCCC TGACCGAGGC ACAA

(2) INFORMATION FOR SEQ. ID NO: 43

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs

 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13-17
- (ix) FEATURES
- (D) OTHER INFORMATION: Tm L3.17 lower primer with Xhol site (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

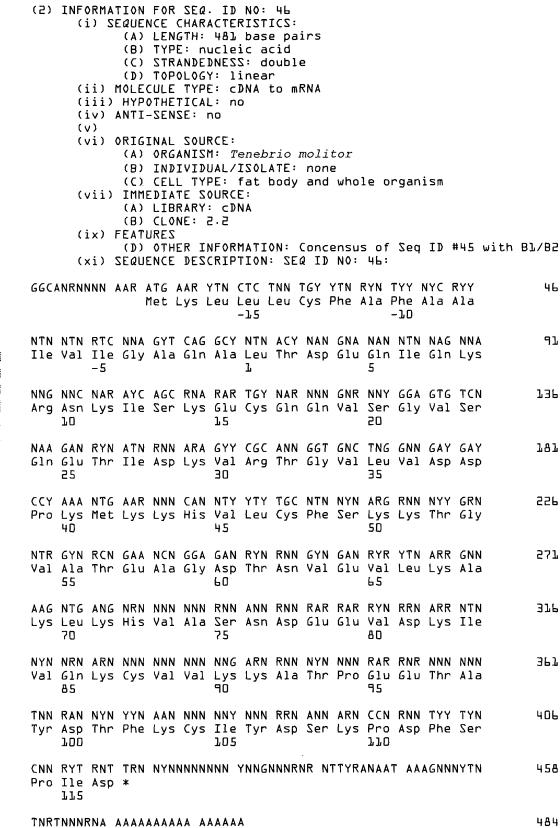
GAGTGGTCAA CTAACTGAGC TCGCC

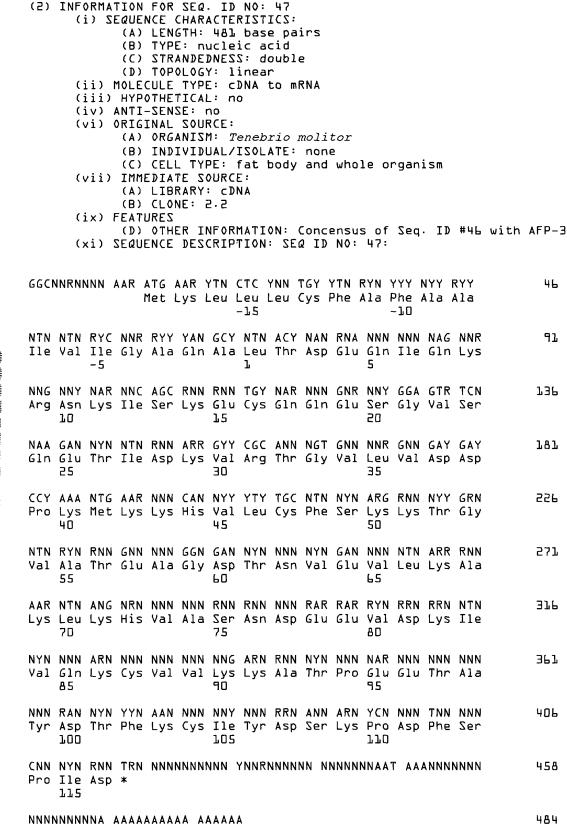
	(5)		i) SI ii) [iii) [iv) [/ii) (EQUEN (A) (D) (D) 10LE HYPO ANTI- CA) (B) (C) IMME (A) (B) (B)	NCE (LENG TYPE STRA TOP(CULE)THE1 -SENS [NAL ORGA IND] CELL EDIA1 LIBF CLON JRES	THARMSTH: THANDER TYPE TICAL SE: SOUP ANISH LVIDE TYPE TY	ACTEN 481 ucle: UNES: Y: 1: I: no RCE: 1: TO UNCE:	RISTI base ic ac S: do inear DNA 1 D eneba Eneba ISOLA fat b E: NA	ICS: pai id ouble to mf	RNA moli: none and	≘ who∶				1.⊒. Au	Isoforms
		()	(i)					TION:					01.2			130.0
	GGC	4CGA(SCA /				_eu l	CTC 1 _eu l -15				Ala f				46
a		GTC Val														91
		AAC Asn 10														136
		GAG Glu 25														787
		AAA Lys 40														556
		GCA Ala 55														571
		CTG Leu 70														316
		AAG Lys 85														3P7
		ACC Thr 100														406
		GAT Asp 115		TTG.	rttt	STA 1	r t t G l	RCTG	4A T'	TTTG,	ACAA'	ΓΑΑ	AGGT	ANTA		455
	TCG	TTAT	SNA /	4444	4444	AA AA	A A A A	A								481

(2) INFORMATION FOR SEQ. ID NO: 45 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 481 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INDIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and whole organism (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: 2.2 (ix) FEATURES													
(D) OTHER INFORMATION: Concensus of Seq ID #44 with Tm l3.l(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:	7												
GGCANRNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYC NYC RYY Met Lys Leu Leu Cys Phe Ala Phe Ala Ala -15 -10													
NTN NTN RTC RNA GYT CAG GCY CTN ACC GAN GNA CAR ATN NAG AAA 91 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys -5 1 5													
NNG AAC AAG ATC AGC AAA RAR TGY CAR NAN GNR NNY GGA GTG TCN Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser 10 15 20													
CAA GAG AYN ATN RNC AAA GYY CGC ANN GGT GNC TNG GNN GAY GAT Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 30 35													
CCY AAA NTG AAR NRN CAN GTY YTY TGC NTN NCN ARG ARN RCY GGN 226 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly 40 45 50													
NTG GCN ACN GAA NCN GGA GAN RYN RNN GTN GAN GTR YTN ARR GNN 271 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala 55 bD b5													
AAG NTG ARG NAN GTN RCY RRC AAC GAC GAA GAR RYN GAN AAR ATC Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile 70 75 80													
RTN NAN AAG TGC GYN GTC AAG ARR GNY ACN NYN GAR GAR ACG GYN Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala 85 90 95													
TNY RAY ACY TTC AAR NNT RTY NNN RAN ARY AAR CCN RAN TTC TCN 40L Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser 100 105													
CCN RTT GAT TRA NYNNYYNNNA YTNGNNNRNR NTTYRANAAT AAAGNNNNTN 458 Pro Ile Asp * 115													

484

TNRTNNNRNA AAAAAAAAA AAAAAA







- (2) INFORMATION FOR SEQ. ID NO: 48
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE:
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Genral Concensus of Clones, Bl, B2 and AFP-3



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

	()	(1) 5	FQUE	NC.	DF7(ו אוא.	TON:	2 E ti	עבי	NV.	40.				
Met	Lys	Leu	Leu	Leu Cys	Cys	Phe Leu	Ile	Phe Ser Leu	Leu	Ala Ile	Ile Leu	Val Leu	Ala	Gly Thr Ala	Val
			-15					-10					-5		
Gln Tyr	Ala	Leu Ile L	Thr	Asp Glu	Ala	Gln Asp Pro	Leu	Gln Glu	Lys Leu	Arg Leu	Asn Arg Lys	Lys Gln 10	Ile Thr His	Ser	Lys Ala Asp
Glu Lys Ala 15	Cys	Gln Lys	Gln Asn Thr Ala	Glu Val	Ser 20	Gly	Val Ala	Ser	Gln Glu	Glu Asp Ala 25	Ile	Ile Leu	Asp Thr Lys Asn	Lys Arg	Val Ala 30
Arg		Arg	Val Asp Glu	Trp		Asp	Asp	Pro	Lys	Met Leu	Lys	Lys Arg Met Glu	His Gln	Val Leu Ala	Leu Phe
				35					40					45	
Cys	Val	Ser Ala Phe Leu	Lys Arg 50	Arg	Ala	Ile	Leu	Ala Val Ile 55	Ala	Glu Ala	Ala Ser	Gly	Asp Glu 60	lle Val	Asn Glu Val Gln
Val Ala Leu	Glu Asp	Thr	Leu Phe Ile	Arg	Ala Glu Thr		Val	Lys Thr Arg	Arg	Asn	Ala Thr Ser	Asn Asp	Asp Asn His	Asp Pro	Glu
		65					70					75			
Glu Lys	Val Ser Thr	Asp Glu	Lys Asp	Ile Leu	Val Ile	Gln Glu Asn Ala	Lys	Cys	Val Ala Thr		Thr	Lys Glu Arg	Ala Asp	Thr	Pro Val
	80					85					90				
Glu Gln	Glu Asp His	Thr Ser	Val	Tyr Phe Ala	Glu	Val	Phe Thr	Lys	Cys Val	Ile Val	Tyr Leu Met His	Asp Lys	Ser Asn Asp	Lys Arg	Pro Ser
95					100					105					770
Asp Asn Lys		Ser Phe	Pro Gly	Ile Asp Val 115	Asp Leu	AAA Phe	^^^ Val	* * *							